

dis his full

(FILE 'HOME' ENTERED AT 09:35:01 ON 25 APR 2007)

FILE 'MEDLINE, BIOSIS, CAPLUS, EMBASE, SCISEARCH, AGRICOLA' ENTERED AT
09:36:18 ON 25 APR 2007

L1 99 SEA ABB=ON PLU=ON ALICYCLOBACILLUS AND PCR
L2 16 SEA ABB=ON PLU=ON L1 AND REAL-TIME
L3 7 DUP REM L2 (9 DUPLICATES REMOVED)
DIS 33 1-7 IBIB
DIS L3 2-7 IBIB
L4 13 SEA ABB=ON PLU=ON L1 AND TAQMAN
DIS L4 ALL IBIB
DIS L4 2-14 IBIB
L5 51 SEA ABB=ON PLU=ON L1 AND 16S
L6 22 DUP REM L5 (29 DUPLICATES REMOVED)
DIS L6 1-22 IBIB

FILE 'STNGUIDE' ENTERED AT 09:48:01 ON 25 APR 2007

FILE HOME

FILE MEDLINE

FILE LAST UPDATED: 24 Apr 2007 (20070424/UP). FILE COVERS 1950 TO DATE.

This file contains CAS Registry Numbers for easy and accurate
substance identification.

FILE BIOSIS

FILE COVERS 1969 TO DATE.

CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNS) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 18 April 2007 (20070418/ED)

FILE CAPLUS

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FILE COVERS 1907 - 25 Apr 2007 VOL 146 ISS 18
FILE LAST UPDATED: 24 Apr 2007 (20070424/ED)

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FILE EMBASE

FILE COVERS 1974 TO 24 Apr 2007 (20070424/ED)

EMBASE is now updated daily. SDI frequency remains weekly (default)
and biweekly.

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FILE SCISEARCH

FILE COVERS 1974 TO 19 Apr 2007 (20070419/ED)

SCISEARCH has been reloaded, see HELP RLOAD for details.

FILE AGRICOLA

FILE COVERS 1970 TO 3 Apr 2007 (20070403/ED)

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FILE STNGUIDE

FILE CONTAINS CURRENT INFORMATION.

LAST RELOADED: Apr 20, 2007 (20070420/UP).

=>

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Sequence Alignments.

1. Sequence alignment of Hristova's primers and probes to the PM1 16S ribosomal RNA gene alignment

963F	1	CCTTGACATGTCTAGAAGTTACCAAGAGA	28
16S	963	CCTTGACATGTCTAGAAGTTACCAAGAGA	990

1076R	1	GCGGGACTTAACCCAACATCT	21
16s	1076	GCGGGACTTAACCCAACATCT	1056

1030T	1	ACACGAGCTGACGACGGCCATG	22
16S	1011	ACACGAGCTGACGACGGCCATG	990

2. Sequence alignments of 10/727261 SEQ ID NOs: 1, 2 and 4:

RESULT 9 (SEQ ID NO: 1) FORWARD PRIMER

ID ADW05721

Qy	1	GAGCCCGCGCGCATTAGC	19
Db	214	GAGCCCGCGCGCATTAGC	232

RESULT 27 (SEQ ID NO: 4) REVERSE PRIMER

ADW05721/c

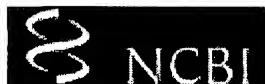
Qy	1	GCTTGCGCCCATTGCG	16
Db	369	GCTTGCGCCCATTGCG	354

RESULT 76 (SEQ ID NO: 2) PROBE

ADW05721

Qy	1	GCGACGATGCGTAGCCG	17
Db	260	GCGACGATGCGTAGCCG	276

3. SEQ ID NO:78 (10/727/261) and Alicyclobacillus and Geobacillus rDNA alignments, and SEQ ID NOs: 1,2 and 4 alignments. See pages (2-9).



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.16 [Mar-25-2007]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x_dropoff: 0 expect: 10.0000 wordsize: 11 Filter View option Standard

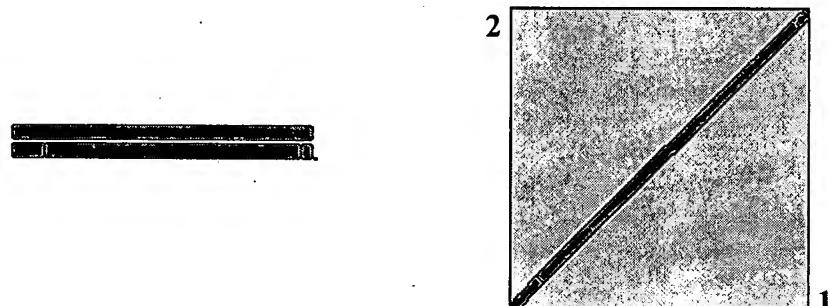
Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation

Sequence 1: lcl|seq_1
Length = 1498 (1 .. 1498)

SEQ 10 # 48

Sequence 2: gi|18496336|dbj|AB042058.1|Alicyclobacillus acidoterrestris gene for 16S ribosomal RNA, partial sequence.
Length = 1514 (1 .. 1514)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 2619 bits (1362), Expect = 0.0
Identities = 1450/1498 (96%), Gaps = 3/1498 (0%)
Strand=Plus/Plus

Query 1	AGAGTTGATCCTGGCTCAGGACGAACGCTGGCGCGTGCCTAATACATGCAAGTCGAGC	60
Sbjct 1	AGAGTTGATCCTGGCTCAGGACGAACGCTGGCGCGTGCCTAATACATGCAAGTCGAGC	60
Query 61	GGGCCCTTCGGGGCCAGCGCGGACGGGTGAGTAACACGTGGTAATCTGCCTTCAGAC	120
Sbjct 61	GAGCCCTTCGGGGCTAGCGCGGACGGGTGAGTAACACGTGGCAATCTGCCTTCAGAC	120
Query 121	CGGAATAACGCCGGAAACGGGTGCTAATGCCGGATANGCACCGAGNAGGCATCTNCTT	180

Sbjct	121	TGGATAACACTCGGAAACGGGTGCTAATGCCGATAAT-ACACGGTAGGCATCTACTT	179
Query	181	GCAGGGAAAGGTGCAANTGCATCGCTGAGAGAGGAGGCCGCGCGCATTAGTAGTTGGT	240
Sbjct	180	GTGTTGAAAGATGCAACTGCATCGCTGAGAGAGGAGGCCGCGCGCATTAGTAGTTGGT	239
Query	241	GGGGTAACGGCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTAGCCGGCACAC	300
Sbjct	240	GAGGTAACGGCTACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTAGCCGGCACAC	299
Query	301	TGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTAGGAAATCTCCGCAATG	360
Sbjct	300	TGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTAGGAAATCTCCGCAATG	359
Query	361	GGCGCAAGCCTGACGGAGCAACGCCGCGTGAGCGAAGAAGGCCCTCGGGTTGAAAGCTC	420
Sbjct	360	GGCGCAAGCCTGACGGAGCAACGCCGCGTGAGCGAAGAAGGCCCTCGGGTTGAAAGCTC	419
Query	421	TGTTGCTCGGGGAGAGCGGCAAGGGAGTGGAAAGCCCTTGNAGACGGTACCGAGTGA	480
Sbjct	420	TGTTGCTCGGGGAGAGCGACAAGGAGAGTGGAAAGCTCCTTGTGAGACGGTACCGAGTGA	479
Query	481	GGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGTAATACGTAGGGGCAAGCGTTGTC	540
Sbjct	480	GGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGTAATACGTAGGGGCAAGCGTTGTC	539
Query	541	CGGAATCACTGGCGTAAAGCGTGCCTAGCGGTTGNGTAAGTCTGGAGTGAAAGTCCAN	600
Sbjct	540	CGGAATCACTGGCGTAAAGCGTGCCTAGCGGTTGNGTAAGTCTGGAGTGAAAGTCCAA	599
Query	601	GGCTCAACCNTGGGAATGCTTGGAAACTGCNTGACTTGAGTGCTGGAGAGGCAAGGGGA	660
Sbjct	600	GGCTCAACCTGGGATTGCTTGGAAACTGCATGACTTGAGTGCTGGAGAGGCAAGGGGA	659
Query	661	ATTCCACGTGTAGCGGTGAAATGCGTAGATATGTGGAGGAATACAGTGGCGAANGCGCC	720
Sbjct	660	ATTCCACGTGTAGCGGTGAAATGCGTAGATATGTGGAGGAATACAGTGGCGAAGGGGCC	719
Query	721	TTGCTGGACAGTGAATGACGCTGAGGCACGAAAGCGTGGGAGCAAACAGGATTAGATAC	780
Sbjct	720	TTGCTGGACAGTGAATGACGCTGAGGCACGAAAGCGTGGGAGCAAACAGGATTAGATAC	779
Query	781	CCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGGGGACACACCCAGTGC	840
Sbjct	780	CCTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGGGGACACACCCAGTGC	839
Query	841	GAAGGAAACCCAATAAGCACTCCGCTGGGAGTACGGTCGAAAGACTGAAACTCAAAGG	900
Sbjct	840	GAAGGAAACCCAATAAGCACTCCGCTGGGAGTACGGTCGAAAGACTGAAACTCAAAGG	899
Query	901	AATTGACGGGGCCCGACAAGCAGTGGAGCATGTGGTTAATTGAAAGCAACGCGAAGA	960
Sbjct	900	AATTGACGGGGCCCGACAAGCAGTGGAGCATGTGGTTAATTGAAAGCAACGCGAAGA	959
Query	961	ACCTTACCAAGGGCTNGACATCCCTCTGACAGCCGAGAGATGGNNTCCCTCGGGCA	1020
Sbjct	960	ACCTTACCAAGGGCTTGACATCCCTCTGACAGCCGAGAGATGGNNTCCCTCGGGCA	1019
Query	1021	GAGGAGACAGGTGGTGCATGGTGTGTCAGCTCGTGTGAGATGTTGGTTAAGTCC	1080